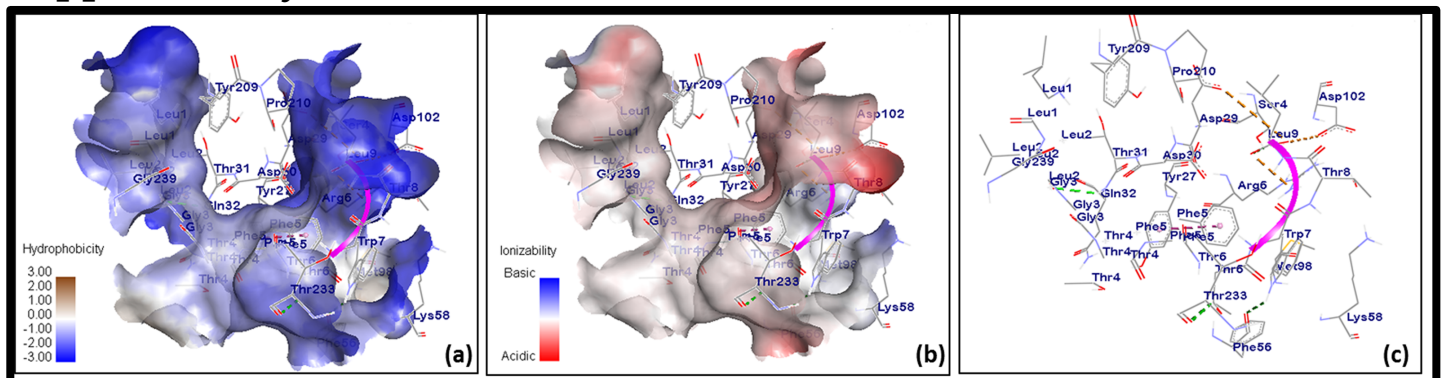
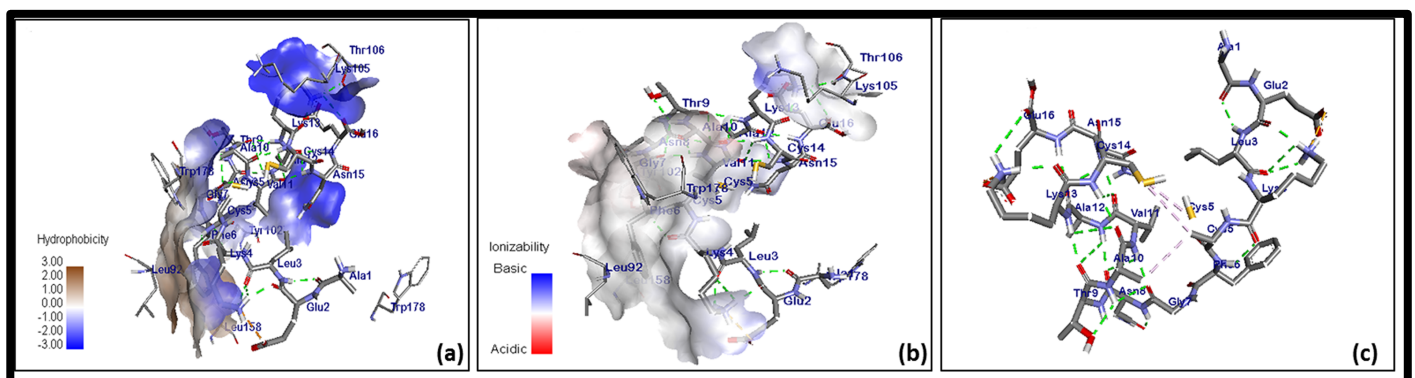


## Supplementary Material:



**Figure S1:** (a) Hydrophobic receptor surface of HLA-A\*02:01 (PDB ID: 3UTQ) and the 'LLGTFWTWL' ligand interaction (b) Ionizable receptor surface of HLA-A\*02:01 (PDB ID: 3UTQ) and the interaction of 'LLGTFWTWL' ligand and (c) Non-bond interaction between HLA-A\*02:01 (PDB ID: 3UTQ) and 'LLGTFWTWL' ligand.



**Figure S2:** (a) Hydrophobic receptor surface of HLA-DRB1\*01:01 (PDB ID: 1AQD) and the 'AELKCFGNTAVAKCNE' ligand interaction (b) Ionizable receptor surface of HLA-DRB1\*01:01 (PDB ID: 1AQD) and the interaction of 'AELKCFGNTAVAKCNE' ligand and (c) Non-bonded interaction between HLA-DRB1\*01:01 (PDB ID: 1AQD) and the 'AELKCFGNTAVAKCNE' ligand.

**Table S1:** Glycoprotein sequences from different strains of LASV at different time frame in different endemic regions

LASV glycoprotein sequences	Accession number
LASVGP_1987	AAA46283.1
LASVGP_1989	AAA46286.1
LASVGP_Josiah_Sep2002	NP_694870.1
LASVGP_Josiah_Dec2010	ADY11068.1
LASVGP_recombinant_Josiah_Dec2010	ADY11070.1
LASVGP_Josiah_Aug2011_Sierra Leone	AEY85213.1
LASVGP_Josiah_Jan2017_Sierra Leone	APT69664.1
LASVGP_Josiah_Jan2017_Sierra Leone	APT69609.1
LASVGP_Jan2017_Guinea	APT69607.1
LASVGP_Josiah_Jan2017_Sierra Leone	APT69605.1
LASVGP_Josiah_Jan2017_Sierra Leone	APT69592.1
LASVGP_Jan2017_Guinea	APT69572.1

**Table S2:** Transmembrane topology analysis of LASV glycoprotein conserved regions using TMHMM v2.0 server

Conserved regions	Nature
1-27	Inner membrane + Transmembrane
29-37	Transmembrane
59-131	Outer membrane
133-173	Outer membrane
175-220	Outer membrane
222-375	Outer membrane
380-409	Outer membrane
411-427	Outer membrane
428-461	Inner + Transmembrane
463-478	Inner membrane

**Table S3:** Results from non-glycosylated T-cell epitope prediction with MHC class I binding score, processing score, proteasomal cleavage score, TAP score interaction along with super-type information is shown.

Sequence	MHC super-type	MHC score	processing score	proteasomal cleavage score	TAP score	Total score
ITEMLQKEY	A1	0.5415	2.2993	0.9549	2.818	2.5834
	B62	0.2637	0.5234	0.9549	2.818	0.8076
LSIPNFNQY	A1	0.3242	1.3764	0.9728	3.015	1.6731
	A26	0.3454	0.927	0.9728	3.015	1.2237
	B58	0.4724	1.0647	0.9728	3.015	1.3614
	B62	0.4597	0.9126	0.9728	3.015	1.2093
LSQRTRDIY	A1	0.2816	1.1957	0.3009	2.985	1.3901
	B62	0.3411	0.6772	0.3009	2.985	0.8716
NWDCIMTSY	A1	0.2562	1.0876	0.8691	3.002	1.368
FSRPSPIGY	A1	0.2354	0.9996	0.7407	2.87	1.2542
	B58	0.3128	0.705	0.7407	2.87	0.9596
	B62	0.5028	0.9981	0.7407	2.87	1.2527
LRDIMGIPY	A1	0.214	0.9087	0.9175	2.936	1.1931
	B27	0.2951	0.7845	0.9175	2.936	1.0689
MRMAWGGSY	A1	0.1321	0.5611	0.8509	3.138	0.8456
	B27	0.5452	1.4493	0.8509	3.138	1.7339
	B62	0.4623	0.9178	0.8509	3.138	1.2023
SLYKGVYEL	A2	0.7619	1.1357	0.9778	1.224	1.3435
	B39	0.3597	1.1517	0.9778	1.224	1.3596
	B62	0.2898	0.5752	0.9778	1.224	0.7831
LLGTFTWTL	A2	0.7622	1.1362	0.9783	0.947	1.3303
RMAWGGSYI	A2	0.6266	0.934	0.9571	0.953	1.1252
	B62	0.4864	0.9656	0.9571	0.953	1.1568
RLDFDNKQA	A2	0.5849	0.8719	0.8557	-0.112	0.9946
CIMTSYQYL	A2	0.5237	0.7806	0.1666	0.968	0.854
IISTFHLSI	A2	0.4681	0.6978	0.6683	0.736	0.348
ALINDQLIM	A2	0.4559	0.6796	0.7948	0.678	0.8327
	A26	0.2836	0.7611	0.7948	0.678	0.9143
	B62	0.3129	0.6213	0.7948	0.678	0.7744
MAWGGSYIA	A2	0.4616	0.688	0.8474	-0.132	0.8086
RLLGTFTWT	A2	0.4924	0.734	0.5216	-0.292	0.7977
MTMPLSCTK	A3	0.6468	1.2174	0.9195	0.696	1.3901
MLRLDFNFK	A3	0.5932	1.1164	0.8549	0.441	1.2667
LINDQLIMK	A3	0.5415	1.0191	0.7773	0.657	1.1686
QMSIQLINK	A3	0.5685	1.0699	0.3017	0.749	1.1526
RTRDIYISR	A3	0.4475	0.8422	0.6413	1.707	1.0238
MLQKEYMER	A3	0.3859	0.7262	0.9385	1.352	0.9346
LMSIISTFH	A3	0.424	0.798	0.0903	-0.26	0.7986
QYEAMSCDF	A24	0.577	1.2286	0.6609	2.809	1.4682
VYELQTLEL	A24	0.5585	1.1893	0.9583	1.107	1.3877
	B39	0.2581	0.8262	0.9583	1.107	1.0246
RWMLIEAEL	A24	0.9396	1.1489	0.9371	1.52	1.3655
TFHLSIPNF	A24	0.5158	1.0982	0.4659	2.765	1.3064
GYCLTRWML	A24	0.4916	1.0467	0.5185	1.019	1.1755
EFCDFMLRLF	A24	0.4277	0.9107	0.1669	2.34	1.0527
	A26	0.4232	1.1357	0.1669	2.34	1.2777
AWGGSYIAL	A24	0.3554	0.7567	0.8072	1.218	0.9387
EGKDTPGGY	A26	0.5752	1.5435	0.9526	2.5060	1.8117
DCIMTSYQY	A26	0.5009	1.3442	0.2989	0.185	1.3983
TTWEDHCQF	A26	0.1784	0.4788	0.9761	2.805	0.7654
SPIGYLGLL	B58	0.5342	1.2039	0.9761	2.805	1.4906
ISRRLLGTF	B8	0.3758	1.2834	0.8407	-0.075	1.4058
LINKAVNAL	B7	0.3062	0.5907	0.782	0.944	0.7552
	B8	0.2316	0.7908	0.374	2.595	0.9766
YISRRLLGT	B8	0.2604	0.8894	0.0430	-0.592	0.8662
RRLGTFFTW	B58	0.3064	0.6906	0.9146	1.0960	0.8826
SIQLINKAV	B8	0.1972	0.6733	0.4906	0.5	0.7719
	B27	0.5307	1.4109	0.9784	1.409	1.628
QRLKAEAQM	B27	0.5114	1.3594	0.8823	0.551	1.5192
KHDEEFCDM	B44	0.2765	0.6853	0.1647	0.944	0.7572

TLELNMETL	B44	0.6825	1.6912	0.3874	0.745	1.7866
HDEEFCMDL	B39	0.256	0.8197	0.6187	0.513	0.9381
	B39	0.21	0.6725	0.9134	0.76	0.8475
AEAQMSIQL	B39	0.2054	0.6577	0.3779	1.081	0.7684
EEFCMDLRL	B44	0.747	1.8512	0.3779	1.081	1.9619
RDIYISRR	B44	0.3093	0.7664	0.4343	0.97	0.88
TEMLQKEYM	B44	0.2782	0.6895	0.609	0.222	0.792
VANGVLQTF	B62	0.3842	0.7628	0.9593	0.904	0.9519
MSIISTFHL	B58	0.6342	1.4293	0.9397	1.159	1.6282
	B58	0.5985	1.3489	0.9048	2.565	1.6128
LQTFMRMAW	B62	0.4276	0.8488	0.2256	2.72	1.0186
SQRTRDIYI	B62	0.3315	0.6581	0.5659	0.76	0.781

**Table S4:** HLA class I specific T-cell epitopes with antigenicity score having IC<sub>50</sub> < 250 nM.

Sequence	Antigenicity score	HLA class I alleles
LLGTFTWTL	0.41022	HLA-A*02:01, HLA-C*12:03, HLA-C*03:03, HLA-B*15:02
RLLGFTFTWT	0.34068	HLA-C*03:03, HLA-C*12:03, HLA-C*14:02, HLA-A*02:06
KHDEEFCDM	0.28311	HLA-C*12:03, HLA-C*05:01, HLA-C*14:02, HLA-C*07:02
RWMLIEAEL	0.24721	HLA-C*12:03, HLA-C*03:03, HLA-C*14:02
SQRTRDIYI	0.2373	HLA-C*12:03, HLA-A*30:01
GYCLTRWML	0.1422	HLA-C*14:02, HLA-C*07:02, HLA-C*12:03, HLA-B*15:02, HLA-C*03:03, HLA-A*23:01
HDEEFCMDL	0.11262	HLA-C*12:03, HLA-C*07:02, HLA-B*15:02, HLA-C*05:01
TTWEDHCQF	0.11152	HLA-C*14:02, HLA-A*32:01, HLA-C*03:03, HLA-C*12:03
LRDIMGIPY	0.10786	HLA-C*12:03, HLA-C*14:02, HLA-C*08:02
MLRLDFDNK	0.23554	HLA-C*12:03, HLA-A*30:01, HLA-C*12:03, HLA-A*03:01, HLA-A*31:01, HLA-A*11:01, HLA-A*68:01
MRMAWGGSY	0.16191	HLA-C*12:03, HLA-C*06:02, HLA-C*07:01, HLA-C*14:02, HLA-B*15:02, HLA-B*27:05, HLA-A*30:02, HLA-A*29:02
RMAWGGSYI	0.15871	HLA-C*03:03, HLA-A*02:01, HLA-C*12:03, HLA-C*14:02, HLA-B*15:02, HLA-A*02:06, HLA-A*32:01
LMSIISTFH	0.15525	HLA-C*03:03, HLA-C*12:03, HLA-C*14:02
RRLLGFTFTW	0.17626	HLA-C*12:03, HLA-A*32:01, HLA-B*58:01, HLA-C*03:03, HLA-B*27:05, HLA-C*07:02
MSIISTFHL	0.17026	HLA-B*15:02, HLA-B*58:01, HLA-A*68:02, HLA-C*12:03, HLA-C*03:03, HLA-A*02:06
LSQRTRDIY	0.19748	HLA-C*12:03, HLA-C*03:03, HLA-B*15:02, HLA-C*14:02, HLA-A*30:02
RTRDIYISR	0.1809	HLA-A*31:01, HLA-A*30:01, HLA-C*12:03, HLA-C*14:02, HLA-A*68:01

**Table S5:** Results from non-glycosylated B-cell epitope prediction using the ABCpred server v2.0. Antigenicity and hydrophilicity were calculated using the IEDB antigen sequence properties tool.

Rank	Sequence	Starting number	ABCpred Score	Antigenicity (IEDB)	Hydrophilicity (IEDB)
01	AELKCFGNTAVAKCNE	288	0.95	1.04	2.431
02	DQLIMKNHLRDMGIP	347	0.90	0.999	0.125
03	LSDSEGKDTGGYCLT	266	0.90	1.007	3.375
04	TEMLQKEYMERQKTP	412	0.89	0.946	3.106
05	EEFCMDLRLDFDNKQA	307	0.88	1.006	0.738
06	WGGSYIALDSGRGNWD	196	0.87	0.957	1.875
07	HLSIPNFNQYEAMSCD	141	0.87	1.027	1.625
08	LGFTFTWLSDSEGKDT	259	0.83	0.963	2.569
09	TFMRMAWGGSYIALDS	190	0.83	0.984	0.081
10	MSIISTFHLSIPNFNQ	134	0.83	1.025	-0.431
11	AEAQMSIQLINKAVNA	328	0.82	1.025	1.331
12	QRTRDIYISRRLLGTF	247	0.81	1.008	0.619
13	TAVAKCNEKHDEEFCD	296	0.80	1.023	3.95
14	KDTPGGYCLTRWMLIE	272	0.78	1.006	0.656
15	YISRRLLGFTFTWLS	253	0.76	1.018	-0.25
16	CLTRWMLIEAELKCFG	279	0.75	1.055	-1.106
17	DHCQFSRPSPIGYLGL	229	0.75	1.067	0.925
18	NQYEAMSCDFNGGKIS	148	0.73	0.981	3.006
19	PLSCTKNNSHHYIMVG	83	0.65	1.047	1.519
20	DFNKQAIQRLKAEAMQ	317	0.63	0.986	2.131
21	RPSPIGYLGLLSQRTR	235	0.62	1.032	0.931
22	YKGVYELQTLLELNMET	62	0.55	1.015	1.181

**Table S6:** MHC class II specific B-cell epitopes having predicted IC<sub>50</sub> less than 250 nM is listed.

Sequence	MHC II HLA
AELKCFGNTAVAKCNE	HLA-DRB1*07:01, HLA-DRB1*01:01, HLA-DRB1*04:04, HLA-DQA1*05:01/DQB1*03:01

LSDSEGKDTPGGYCLT	Nil
HLSIPNFNQYEAMSCD	HLA-DRB1*01:01
AEAQMSIQLINKAVNA	HLA-DRB4*01:01, HLA-DRB1*01:01, HLA-DRB1*04:04, HLA-DRB1*11:01
PLSCTKNNSSHYYIMVG	Nil
YKGVYELQTLLELNMET	HLA-DRB1*01:01, HLA-DRB1*04:05, HLA-DPA1*02:01/DPB1*01:01, HLA-DPA1*03:01/DPB1*04:02
TAVAKCNEKHDEEFCF	Nil

**Table S7:** Population coverage of class I MHC specific T-cell epitopes

Population/area	Class I		
	Coverage	Average hit	pc90
Central Africa	18.78%	0.36	0.12
East Africa	23.39%	0.31	0.13
East Asia	38.61%	0.45	0.16
Europe	59.02%	1.15	0.24
North Africa	34.05%	0.69	0.15
North America	49.7%	0.72	0.2
Northeast Asia	26.32%	0.43	0.14
Oceania	27.89%	0.44	0.14
South America	28.08%	0.44	0.14
South Asia	21.92%	0.54	0.13
Southeast Asia	23.07%	0.29	0.13
Southwest Asia	33.69%	0.61	0.15
West Africa	22.14%	0.33	0.13
West Indies	32.19%	0.32	0.15
World	50.04%	0.88	0.2

**Table S8:** Population coverage of class II MHC specific B-cell epitopes

Population/area	Class II		
	Coverage	Average hit	pc90
Central Africa	15.2%	0.17	0.12
Central America	12.49%	0.14	0.11
East Africa	12.76%	0.17	0.11
East Asia	17.28%	0.28	0.12
Europe	36.78%	0.54	0.16
North Africa	27.63%	0.3	0.14
North America	31.49%	0.46	0.15
Northeast Asia	10.91%	0.14	0.11
Oceania	2.67%	0.03	0.1
South America	13.17%	0.17	0.12
South Asia	36.27%	0.47	0.16
Southeast Asia	7.13%	0.08	0.11
Southwest Asia	14.43%	0.17	0.12
West Africa	12.69%	0.17	0.11
West Indies	26.71%	0.37	0.14
World	28.63%	0.41	0.14